SEQUENCE LISTING

<110> Martin Richard

Flatt Brenton Todd

Kahl Jeffrey Dean Wang Tie-Lin <120> HETEROCYCLIC MODULATORS OF NUCLEAR RECEPTORS <130> 38205-3001B <140> Unassigned <141> Herewith <150> 10/329,668 <151> 2002-12-20 <150> 60/342,720 <151> 2001-12-21 <160> 18 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1528 <212> DNA <213> Homo Sapien <220> <221> CDS <222> (36)...(1379) <300> <308> GeneBank Nm 005693 <309> 2002-05-14 <400> 1 cagtgccttg gtaatgacca gggctccaga aagag atg tcc ttg tgg ctg ggg 53 Met Ser Leu Trp Leu Gly gcc cct gtg cct gac att cct cct gac tct gcg gtg gag ctg tgg aag Ala Pro Val Pro Asp Ile Pro Pro Asp Ser Ala Val Glu Leu Trp Lys 101 10 149 Pro Gly Ala Gln Asp Ala Ser Ser Gln Ala Gln Gly Gly Ser Ser Cys 25 atc ctc aga gag gaa gcc agg atg ccc cac tct gct ggg ggt act gca 197 Ile Leu Arg Glu Glu Ala Arg Met Pro His Ser Ala Gly Gly Thr Ala ggg gtg ggg ctg gag gct gca gag ccc aca gcc ctg ctc acc agg gca Gly Val Gly Leu Glu Ala Ala Glu Pro Thr Ala Leu Leu Thr Arg Ala gag ccc cct tca gaa ccc aca gag atc cgt cca caa aag cgg aaa aag 293 Glu Pro Pro Ser Glu Pro Thr Glu Ile Arg Pro Gln Lys Arg Lys 80 ggg cca gcc ccc aaa atg ctg ggg aac gag cta tgc agc gtg tgt ggg Gly Pro Ala Pro Lys Met Leu Gly Asn Glu Leu Cys Ser Val Cys Gly 341

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Gly Pro Glu Pro Trp Pro Gly Gly Pro Asp Pro Asp Val Pro Gly Thr
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							Gly 999									538
							aag Lys									586
							gtg Val 185									634
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							gcc Ala									778
							acg Thr									826
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							atc Ile									922
							gag Glu									970
							cta Leu									1018
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							cag Gln 345									1114
							cgg Arg									1162

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Gln Glu Pro Gly Arg Val Glu Ala Leu Gln Gln Pro Tyr Val Glu Ala
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Leu Leu Ser Tyr Thr Arg Ile Lys Arg Pro Gln Asp Gln Leu Arg Phe
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Pro Arg Met Leu Met Lys Leu Val Ser Leu Arg Thr Leu Ser Ser Val
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		gag Glu														513
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		ggg Gly														609
		cga Arg														657
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					gaa Glu											644
					gta Val											692
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Gly 333	tgt Cys	aaa Lys	ggt Gly	ttc Phe 150	ttc Phe	agg Arg	aga Arg	agc Ser	att Ile 155	acc Thr	aaa Lys	aac Asn	gct Ala	gtg Val 160	tac Tyr	836
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cca gga Pro Gl	ttt c	ag act In Thr 310	ttg gad Leu Asp	cat His	gaa Glu	gac Asp 315	cag Gln	att Ile	gct Ala	ttg Leu	ctg Leu 320	aaa Lys	1316
	Ala V		gct atg Ala Met										1364
			ggg cat Gly His										1412
	Gly I		gat gaa Asp Glu 360	Tyr									1460
			ctg aaa Leu Lys 375										1508
			ctg tct Leu Ser										1556
	val G		ctt cag Leu Gln										1604
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Leu Gly		eu Thr	gaa tta Glu Leu 440	Arg		Phe	Asn	His	His				1700
			aga gta Arg Val 455										1748
tgt gaa Cys Gli	atc to	gg gac rp Asp 470	gtg cag Val Gln	tga *	tggg	ggatt	cac a	3 9999	gaggg	gg to	ctago	ctcct	1802
actcaag aatattg ctgcatt ctgttga agagttg	gaaa tc gggc tag ccta at act agg gtat tc aaaa aa	ttgatga gatagaa tggcaaq ggaaaat aatcttq	te tgatgaa tatttae aacttge cetgte teattgg caataaa aaaaa	atgti tctci ttgci ttgci aagci	t gta t aca c taa t cat a aaa	aatta attgt attaa cctta cataa	acat gtt aatt acca atgg	gtgt ttaa gatt tatt caa	aact aaagg gtta gcat cagaa	get of act the same act to act	cacaa ccago ccaat atttt aaaaa	actgta ggaatc tctat tattaa aaaaaa	1922 1982 2042 2102

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                                                                       158
                                                                       206
ccc tcg ctg cac ccg tcc ctg ggg cct ggc atc ggc tcc ccg gga cag
Pro Ser Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln
ctg cat tot occ atc ago acc ctg ago too occ atc aac ggc atg ggc
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Leu His Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly
ceg cet the teg give ate age the ece atg gge eee can tee atg teg
                                                                        302
Pro Pro Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser
gtg ccc acc acc ccc acc ctg ggc ttc agc act ggc agc ccc cag ctc
Val Pro Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu
     80
age tea cet atg aac eec gte age age gag gae ate aag eec eec
                                                                       398
Ser Ser Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro
ctg ggc ctc aat ggc gtc ctc aag gtc ccc gcc cac ccc tca gga aac
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Leu Gly Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn
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atg gct tcc ttc acc aag cac atc tgc gcc atc tgc ggg gac cgc tcc
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                                   135
tca ggc aag cac tat gga gtg tac agc tgc gag ggg tgc aag ggc ttc
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Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe
ttc aag cgg acg gtg cgc aag gac ctg acc tac acc tgc cgc gac aac
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Phe Lys Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn
    160
aag gac tgc ctg att gac aag cgg cag cgg aac cgg tgc cag tac tgc
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Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys
cgc tac cag aag tgc ctg gcc atg ggc atg aag cgg gaa gcc gtg cag
Arg Tyr Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln
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	Ser				gag Glu											1262
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					ctc Leu 420											1358
					ctc Leu											1406
					atg Met											1454
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Thr Glu Ser Pro Ile Cys Pro Leu Ser Pro Leu Glu Ala Asp Asp Leu
                                                                      271
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Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly Asn Ile Gln
gag att tot cag too ato ggt gag gag ago tot gga ago tit ggt tit
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Glu Ile Ser Gln Ser Ile Gly Glu Glu Ser Ser Gly Ser Phe Gly Phe
gca gac tac cag tac tta gga agc tgt ccg ggc tcc gag ggc tct gtc
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Ala Asp Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Glu Gly Ser Val
                                                                      415
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Ile Thr Asp Thr Leu Ser Pro Arg Ser Ser Pro Ser Ser Val Ser Cys
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Pro Val Ile Pro Ala Ser Thr Asp Glu Ser Pro Gly Ser Ala Leu Asn
atc gag tgt cga ata tgt ggg gac aag gcc tca ggg tac cac tac gga
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Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr His Tyr Gly
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                                          110
                                                                      559
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Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg
ctg aag ctg gtg tac gac aag tgt gat cgg agc tgc aag att cag aag
Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys Ile Gln Lys
                                                                      607
aag aac cgg aac aaa tgc cag tac tgc cgt ttt cac aag tgc ctg tct
                                                                      655
Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys Cys Leu Ser
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                                                  160
gtc ggg atg tca cac aat gca att cgc ttt gga aga atg cca aga tct
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Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Arg Ser
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Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu His Asp Leu
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							acc Thr									1039
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							gtg Val									1327
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<213> Mus musculus

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Cys Gly Asp Arg Pro Gly Leu Leu Asn Ile Gly Tyr Ile Glu Lys Leu 390 395 Gln Glu Gly Ile Val His Val Leu Lys Leu His Leu Gln Ser Asn His 405 410 415 Pro Asp Asp Thr Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Val Asp 420 425 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Val Ile Lys 435 440 445 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr 455 Arg Asp Met Tyr <210> 13 <211> 1323 <212> DNA <213> Mus musculus <220> <221> CDS <222> (1)...(1323) <300> <308> GeneBank U10375 <309> 1994-07-22 <400> 13 atg gaa cag cca cag gag gag acc cct gag gcc cgg gaa gag gag aaa 48 Met Glu Gln Pro Gln Glu Glu Thr Pro Glu Ala Arg Glu Glu Glu Lys gag gaa gtg gcc atg ggt gac gga gcc ccg gag ctc aat ggg gga cca Glu Glu Val Ala Met Gly Asp Gly Ala Pro Glu Leu Asn Gly Gly Pro 96 gaa cac acg ctt cct tcc agc agc tgt gca gac ctc tcc cag aat tcc 144 Glu His Thr Leu Pro Ser Ser Ser Cys Ala Asp Leu Ser Gln Asn Ser 40 35 192 tee cet tee tee etg etg gae eag etg eag atg gge tgt gat ggg gee Ser Pro Ser Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly Ala 55 50 tca ggc ggc agc ctc aac atg gaa tgt cgg gtg tgc ggg gac aag gcc Ser Gly Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys Ala teg gge tte cae tae ggg gte cae geg tge gag ggg tge aag gge tte Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe ttc cgc cgg aca atc cgc atg aag ctc gag tat gag aag tgc gat cgg Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Asp Arg 336 105 384 atc tgc aag atc cag aag aag cgc aac aag tgt cag tac tgc cgc Ile Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg ttc cag aag tgc ctg gca ctc ggc atg tcg cac aac gct atc cgc ttt Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe 432 130 135 gga cgg atg ccg gac ggc gag aag agg aag ctg gtg gcg ggg ctg act Gly Arg Met Pro Asp Gly Glu Lys Arg Lys Leu Val Ala Gly Leu Thr 150 155 160

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Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg Phe 130 135 140
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Ala Ser Glu Gly Cys Gln His Asn Pro Gln Leu Ala Asp Leu Lys Ala
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Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met Thr

Lys Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ser Ser His Asn Ala
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200
205

Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys Gly
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Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Asn Glu Ile

225 230 235 240

Ser Val His Val Phe Tyr Arg Cys Gln Ser Thr Thr Val Glu Thr Val

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Arg Glu Leu Thr Glu Phe Ala Lys Asn Ile Pro Asn Phe Ser Ser Leu 260 270
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777

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Ser Gly Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe

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	tat Tyr															921
	gaa Glu															969
	acc Thr															1017
	ctt Leu															1065
	aac Asn 260															1113
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	gac Asp															1209
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	agt Ser 340															1353
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	cga Arg															1449
	tct Ser															1497
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	ctg Leu 420															1593

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Phe Leu Met Glu Met Leu Glu Thr Pro Leu Gln Ile Thr
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Lys Pro Leu Pro Gly Leu Pro Gly Ile Gly Asn Met Asn Tyr Pro Ser
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Asp Asn Lys Asp Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln
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Tyr Cys Arg Tyr Gln Lys Cys Leu Val Met Gly Met Lys Arg Glu Ala
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Ala Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro
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His Phe Ser Asp Leu Thr Leu Glu Asp Gln Val Ile Leu Leu Arg Ala
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Cys Leu Glu His Leu Phe Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile
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Cys Pro Pro Pro Gly Gly Pro Gly Ala Gly Lys Arg Leu Cys Ala
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Gln Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Gly Thr Gly Gly Ser
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